

SEQUENCE LISTING

<110> KOSUGI, Yoshinori
KURODA, Masahiko
OIKAWA, Kosuke
OHBAYASHI, Tetsuya

<120> METHOD OF DIAGNOSING DISEASES RELATING TO ENDOMETRIOSIS

<130> 2006-0026A/WMC/00653

<140> 10/564,484

<141> 2006-01-13

<150> JP2003-196455

<151> 2003-07-14

<160> 10

<170> PatentIn version 3.1

<210> 1

<211> 830

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (95)..(613)

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ctagcgccgt cgtcgtctcc cttcagtcgc catc atg att atc tac cgg gac ctc 115
Met Ile Ile Tyr Arg Asp Leu
1 5

atc agc cac gat gag atg ttc tcc gac atc tac aag atc cgg gag atc 163
Ile Ser His Asp Glu Met Phe Ser Asp Ile Tyr Lys Ile Arg Glu Ile
10 15 20

gcg gac ggg ttg tgc ctg gag gtg gag ggg aag atg gtc agt agg aca 211
Ala Asp Gly Leu Cys Leu Glu Val Glu Gly Lys Met Val Ser Arg Thr
25 30 35

gaa ggt aac att gat gac tcg ctc att ggt gga aat gcc tcc gct gaa 259
Glu Gly Asn Ile Asp Asp Ser Leu Ile Gly Gly Asn Ala Ser Ala Glu
40 45 50 55

ggc ccc gag ggc gaa ggt acc gaa agc aca gta atc act ggt gtc gat 307
Gly Pro Glu Gly Glu Gly Thr Glu Ser Thr Val Ile Thr Gly Val Asp
60 65 70

att gtc atg aac cat cac ctg cag gaa aca agt ttc aca aaa gaa gcc 355
Ile Val Met Asn His His Leu Gln Glu Thr Ser Phe Thr Lys Glu Ala
75 80 85

tac aag aag tac atc aaa gat tac atg aaa tca atc aaa ggg aaa ctt 403
Tyr Lys Lys Tyr Ile Lys Asp Tyr Met Lys Ser Ile Lys Gly Lys Leu
90 95 100

gaa gaa cag aga cca gaa aga gta aaa cct ttt atg aca ggg gct gca 451
Glu Glu Gln Arg Pro Glu Arg Val Lys Pro Phe Met Thr Gly Ala Ala
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105	110	115	
gaa caa atc aag cac atc ctt gct aat ttc aaa aac tac cag ttc ttt Glu Gln Ile Lys His Ile Leu Ala Asn Phe Lys Asn Tyr Gln Phe Phe 120 125 130 135			499
att ggt gaa aac atg aat cca gat ggc atg gtt gct cta ttg gac tac Ile Gly Glu Asn Met Asn Pro Asp Gly Met Val Ala Leu Leu Asp Tyr 140 145 150			547
cgt gag gat ggt gtg acc cca tat atg att ttc ttt aag gat ggt tta Arg Glu Asp Gly Val Thr Pro Tyr Met Ile Phe Phe Lys Asp Gly Leu 155 160 165			595
gaa atg gaa aaa tgt taa caaatgtggc aattattttg gatctatcac Glu Met Lys Cys 170			643
ctgtcatcat aactggcttc tgcttgtcat ccacacaaca ccaggactta agacaaatgg			703
gactgatgtc atcttgagct cttcatttat tttgactgtg atttatttgg agtggaggca			763
ttgttttttaa gaaaaacatg tcatgtaggt tgtctaaaaa taaaatgcat ttaaactcat			823
ttgagag			830

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 20 25 30
 Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
 35 40 45
 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
 50 55 60
 Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
 65 70 75 80
 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
 85 90 95
 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
 100 105 110
 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
 115 120 125
 Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
 130 135 140
 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met
 145 150 155 160
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 165 170

<210> 3
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<210> 4
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<212> DNA
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<210> 9
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